

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 7, 2005, 06:56:21 ; Search time 96.4051 Seconds

(without alignments)  
1349.183 Million cell updates/sec

Title: US-09-939-537-33

Perfect score: 1385  
Sequence: 1 EFKSCDKHTCPPCAPBL.....DETCAMAGDGLDGLTTDP 254

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1356	97.9	544	2	Q6PJ95
2	1255	91.3	509	2	Q6PJ95
3	1258	90.8	330	1	GCI_HUMAN
4	1258	90.8	465	2	Q6GKX6
5	1258	90.8	466	2	Q6GKX6
6	1258	90.8	469	2	Q6GKX6
7	1258	90.8	470	2	Q6GKX6
8	1258	90.8	472	2	Q6GKX6
9	1258	90.8	472	2	Q6GKX6
10	1258	90.8	475	2	Q6GKX6
11	1258	90.8	476	2	Q6GKX6
12	1258	90.8	479	2	Q6GKX6
13	1254	90.5	473	2	Q6GKX6
14	1254	90.5	475	2	Q6GKX6
15	1254	90.5	480	2	Q6GKX6
16	1254	90.5	481	2	Q6GKX6
17	1254	90.5	482	2	Q6GKX6
18	1252	90.4	438	2	Q6GKX6
19	1252	90.4	473	2	Q6GKX6
20	1252	90.4	478	2	Q6GKX6
21	1252	90.4	480	2	Q6GKX6
22	1251	90.3	466	2	Q6GKX6
23	1247	90.0	475	2	Q6GKX6
24	1247	90.0	487	2	Q6GKX6
25	1171	84.5	354	2	Q6GKX6
26	1171	84.5	358	2	Q6GKX6
27	1167	84.3	521	2	Q6GKX6
28	1151	83.1	320	1	GCI_HUMAN
29	1140	82.3	417	2	Q6GKX6
30	1140	82.3	417	2	Q6GKX6
31	1137	82.1	464	2	Q6GKX6

32	1135	81.9	465	2	Q6P6C4
33	1130	81.6	327	1	GCI_HUMAN
34	1130	81.6	473	2	Q6P6C3
35	1126	81.3	493	2	Q6GKX4
36	1121	80.9	476	2	Q6GKX7
37	938.5	67.8	303	2	Q6KAM2
38	938.5	67.8	398	1	GCI_MOUSE
39	931.5	67.3	393	1	GCI_MOUSE
40	916	66.1	323	1	GC_RABIT
41	910.5	65.7	337	2	Q6GKX4
42	905	65.3	399	1	GCI_MOUSE
43	896	64.7	429	1	GCI_MOUSE
44	870.5	62.9	305	1	GCI_MOUSE
45	840.5	60.7	329	1	GCI_MOUSE

## ALIGNMENTS

RESULT 1  
ID Q6PJ95 PRELIMINARY; PRT; 544 AA.  
AC Q6PJ95;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SOURCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Spauldy S.J., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pangloss S.J., Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywicki M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E., Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
EMBL BC019046; AAH19046.1; -;  
HSSP: P01861; IADO.  
DR InterPro: IPR003599; IG.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003597; IG-cl.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_v.  
DR Pfam: PF07654; Cl-seq; 3.  
DR SMART: SM00409; IG\_2.  
DR SMART: SM00407; IGcl; 3.  
DR SMART: SM00406; IGv; 1.  
DR PROSITE: PS00835; IG LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.

KW Hypothetical protein.  
 SQ SEQUENCE 544 AA; 60102 MW; 1895814B2297C668 CRC64;  
 Query Match 97.9%; Score 1356; DB 2; Length 544;  
 Best Local Similarity 98.8%; Pred. No. 1.1e-97;  
 Matches 249; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVYTCVVVDVSHEDPEVKF 60  
 DB 244 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVYTCVVVDVSHEDPEVKF 303  
 QY 61 NMVVDGVEVNAKTKPREEQNTSTYRVSVLTVLDQMLNGKEVKCKVSKNKAALPAPIEKT 120  
 DB 304 NMVVDGVEVNAKTKPREEQNTSTYRVSVLTVLDQMLNGKEVKCKVSKNKAALPAPIEKT 363  
 QY 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 180  
 DB 364 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 423  
 QY 181 PVLDSGSEFLYSKLTVDKSRWQQGNVFCSVVMEALHNHYTQKSLSFGLDPTCAE 240  
 DB 424 PVLDSGSEFLYSKLTVDKSRWQQGNVFCSVVMEALHNHYTQKSLSFGLDPTCAE 483  
 QY 241 AODGELDGLMTT 252  
 DB 484 AODGELDGLMTT 495

RESULT 2  
 ID Q8NF17 PRELIMINARY; PRT; 509 AA.  
 AC Q8NF17;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 GN P1J00385 Protein (Fragment).  
 GN Name=P1J00385;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.,  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK090464; BAC03445.1; -.  
 DR PIR; A45874; A45874.  
 DR HSP; P01842; 7PAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_C1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF07654; C1-set; 3.  
 DR SMART; SM00407; IG1; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS00230; IG\_MHC; UNKNOWN 2.  
 DR NON TER  
 FT  
 SQ SEQUENCE 509 AA; 56110 MW; 089498D8076B863C CRC64;

Query Match 91.3%; Score 1265; DB 2; Length 509;  
 Best Local Similarity 91.7%; Pred. No. 1.3e-90;  
 Matches 231; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVYTCVVVDVSHEDPEVKF 60  
 DB 209 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVYTCVVVDVSHEDPEVKF 268  
 QY 61 NMVVDGVEVNAKTKPREEQNTSTYRVSVLTVLDQMLNGKEVKCKVSKNKAALPAPIEKT 120  
 DB 269 NMVVDGVEVNAKTKPREEQNTSTYRVSVLTVLDQMLNGKEVKCKVSKNKAALPAPIEKT 328  
 QY 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 180  
 DB 328 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 387

DB 329 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTP 388  
 QY 181 PVLDSGSEFLYSKLTVDKSRWQQGNVFCSVVMEALHNHYTQKSLSFGLDPTCAE 240  
 DB 389 PVLDSGSEFLYSKLTVDKSRWQQGNVFCSVVMEALHNHYTQKSLSFGLDPTCAE 448  
 QY 241 AODGELDGLMTT 252  
 DB 449 AODGELDGLMTT 460

RESULT 3  
 ID GCI\_HUMAN STANDARD; PRT; 330 AA.  
 AC P01857;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Ig gamma-1 chain C region.  
 GN Name=IGHG1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=82274238; PubMed=6287432;  
 RA Ellison J.W., Berson B.J., Hood L.E.;  
 RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";  
 RL Nucleic Acids Res. 10:4071-4079(1982).  
 RN [2]  
 RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
 RC MEDLINE=71064024; PubMed=5489771;  
 RA Cunningham B.A., Rutishauser U., Gail W.E., Gottlieb P.D.,  
 RA Waxdal M.J., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
 RL Biochemistry 9:3161-3170(1970).  
 RN [3]  
 RP SEQUENCE OF 136-329 (EU).  
 RC MEDLINE=71064025; PubMed=5530842;  
 RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
 RA Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
 RL Biochemistry 9:3171-3181(1970).  
 RN [4]  
 RP SEQUENCE (MYELOMA PROTEIN NIE).  
 RC MEDLINE=77070269; PubMed=826475;  
 RA Ponstingl H., Hilschmann N.;  
 RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
 RN [5]  
 RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
 RC MEDLINE=83289131; PubMed=6884994;  
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
 RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
 RN [6]  
 RP DISULFIDE BONDS.  
 RC MEDLINE=71064027; PubMed=4923144;  
 RA Gail W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";  
 RL Biochemistry 9:3188-3196(1970).  
 RN [7]  
 RP DISULFIDE BONDS.  
 RC MEDLINE=77070267; PubMed=1002129;  
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;

RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and  
 RT characterization of the protein, the L- and H-chains, the cyanogen  
 RT bromide cleavage products, and the disulfide bridges";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540 (1976).  
 RN (8)  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=81208100; Pubmed=7236608;  
 RA Deisenhofer J.;  
 RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from Staphylococcus  
 RT aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370 (1981).  
 CC -1- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the  
 CC G1M(1) marker, 239-D and 241-L. KOL and EU sequences have the  
 CC G1M(3) marker and the G1M (non-1) markers.  
 CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35,  
 CC 116, 198, 269 and 272.  
 CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues  
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
 CC 268-272.  
 CC -1- MISCELLANEOUS: KOL also differs in the amidation states of  
 CC residues 198, 267 and 272.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, J00238; AAC82527.1; ALT\_INIT.  
 DR PIR, A93433; GHNU.  
 DR PDB: 1A7J; X-ray; H=1-103.  
 DR PDB: 1D5B; X-ray; B/H=1-101.  
 DR PDB: 1D5I; X-ray; H=1-101.  
 DR PDB: 1D6V; X-ray; H=1-101.  
 DR PDB: 1DN2; X-ray; A/B=120-326.  
 DR PDB: 1EAK; X-ray; A/B=106-329.  
 DR PDB: 1FC1; X-ray; A/B=106-329.  
 DR PDB: 1FC2; X-ray; D=106-329.  
 DR PDB: 1FCC; X-ray; A=121-326.  
 DR PDB: 1H2H; X-ray; H/K=1-330.  
 DR PDB: 1I7Z; X-ray; B/D=1-103.  
 DR PDB: 1I1S; X-ray; A/B=107-330.  
 DR PDB: 1I1X; X-ray; A/B=107-330.  
 DR PDB: 1L6X; X-ray; A=120-326.  
 DR PDB: 1OQX; X-ray; A/B=119-330.  
 DR PDB: 2RCS; X-ray; H=1-103.  
 DR Genew; HGNC:5525; IGHG1.  
 DR MIM; 147100; -.  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; F:antigen binding; TAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_3.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 DR 3D-structure; Direct protein sequencing; Glycoprotein;  
 KW Immunoglobulin C region; Immunoglobulin domain.  
 KM  
 FT NON\_TER 1 1  
 FT DOMAIN 1 98 CH1.  
 FT DOMAIN 99 110 Hinge.  
 FT DOMAIN 111 223 CH2.  
 FT DOMAIN 224 330 CH3.  
 FT DISULFID 27 83  
 FT DISULFID 103 103 Interchain (with light chain).  
 FT DISULFID 109 109 Interchain (with heavy chain).  
 FT DISULFID 112 112 Interchain (with heavy chain).  
 FT DISULFID 144 204  
 FT DISULFID 250 308

FT CARBOHYD 180 180 N-linked (GlcNAc...)  
 FT VARIANT 97 97 K -> R (in G1M(3) marker).  
 FT VARIANT 239 239 /FTid=VAR\_003886.  
 FT VARIANT 241 241 D -> E (in G1M(non-1) marker).  
 FT VARIANT 241 241 /FTid=VAR\_003887.  
 FT VARIANT 241 241 L -> M (in G1M(non-1) marker).  
 FT VARIANT 241 241 /FTid=VAR\_003888.  
 FT STRAND 23 24  
 FT STRAND 26 33  
 FT STRAND 38 38  
 FT STRAND 41 41  
 FT STRAND 41 41  
 FT STRAND 42 45  
 FT STRAND 48 49  
 FT STRAND 50 52  
 FT STRAND 57 58  
 FT STRAND 59 61  
 FT STRAND 62 71  
 FT STRAND 73 75  
 FT STRAND 76 78  
 FT STRAND 82 87  
 FT STRAND 88 91  
 FT STRAND 92 97  
 FT STRAND 102 103  
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 FT STRAND 157 162  
 FT STRAND 163 164  
 FT STRAND 165 167  
 FT STRAND 172 172  
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 FT STRAND 238 242  
 FT STRAND 245 256  
 FT STRAND 261 266  
 FT STRAND 267 268  
 FT STRAND 269 270  
 FT STRAND 274 276  
 FT STRAND 280 281  
 FT STRAND 283 284  
 FT STRAND 287 296  
 FT STRAND 297 301  
 FT STRAND 302 303  
 FT STRAND 306 311  
 FT STRAND 313 314  
 FT STRAND 316 318  
 FT STRAND 319 324  
 FT STRAND 324 324  
 SQ SEQUENCE 330 AA; 36106 MW; 3770EB106C2FA33D CRC64;  
 Query Match 90.8%; Score 1258; DB 1; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-90;  
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EPKSCDKHTCPCPAPPELLGGPSVFLPPPKRDITLMSRTPEVTCVVVDVSHEDPEVKF 60  
 DB 99 EPKSCDKHTCPCPAPPELLGGPSVFLPPPKRDITLMSRTPEVTCVVVDVSHEDPEVKF 158  
 QY 61 NMYVDGVEVHNAKTPRERQYNSTYRVVSVLTVTHQDMLNGKEYCKYKNKALPAPIEKT 120  
 DB 159 NMYVDGVEVHNAKTPRERQYNSTYRVVSVLTVTHQDMLNGKEYCKYKNKALPAPIEKT 218  
 QY 121 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180  
 DB 219 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 278

QY 181 PVLDSGSPFLYSKLTVDKSRWQGNVFCSCVWHEALNHNHYOKSLISLSPG 231  
Db 279 PVLDSGSPFLYSKLTVDKSRWQGNVFCSCVWHEALNHNHYOKSLISLSPG 329

## RESULT 4

OG6MX6 PRELIMINARY; PRT; 465 AA.  
AC OG6MX6;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
OC Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marisela K., Farmer A.A., Rubin G.M., Hong L.,  
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RX Strauberg R.,  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC073766; AAH73766.1; -.  
DR InterPro: IPR003599; IG.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003597; IG.C1.  
DR InterPro: IPR003006; IG.MHC.  
DR InterPro: IPR003596; IG.V.  
DR Pfam: PF07654; C1-set; 3.  
DR Pfam: PF00047; Ig; 4.  
DR SMART: SM00409; Ig; 2.  
DR SMART: SM00407; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG.LIKE; 4.  
DR PROSITE: PS00290; IG.MHC; UNKNOWN 2.  
DR Hypothetical protein.  
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 90.8%; Score 1258; DB 2; Length 465;  
Best Local Similarity 100.0%; Pred. No. 4,1e-90;  
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHICPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
Db 234 EPKSCDKTHICPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 293  
QY 61 NMVYDGEVHNAKTRPREQYNSTRVSVLTTLHODMNGKEYCKVSNKALPAPIEKT 120  
|||||

Db 294 NMVYDGEVHNAKTRPREQYNSTRVSVLTTLHODMNGKEYCKVSNKALPAPIEKT 353

QY 121 ISKAKQPREPOVYTLPPSRDELTRKNQVSLTCLVKGFPSDIAVEWESNGOENNYKTP 353

Db 354 ISKAKQPREPOVYTLPPSRDELTRKNQVSLTCLVKGFPSDIAVEWESNGOENNYKTP 180

QY 181 PVLDSGSPFLYSKLTVDKSRWQGNVFCSCVWHEALNHNHYOKSLISLSPG 231  
Db 414 PVLDSGSPFLYSKLTVDKSRWQGNVFCSCVWHEALNHNHYOKSLISLSPG 464

## RESULT 5

OG6IN78 PRELIMINARY; PRT; 466 AA.  
AC OG6IN78;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
OC IG1G1 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Peripheral Nervous System;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marisela K., Farmer A.A., Rubin G.M., Hong L.,  
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Peripheral Nervous System;  
RX Strauberg R.,  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC072419; AAH72419.1; -.  
DR HSP: P01861; IAD0.  
DR InterPro: IPR007110; IG.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003597; IG.C1.  
DR InterPro: IPR003006; IG.MHC.  
DR InterPro: IPR003596; IG.V.  
DR Pfam: PF07654; C1-set; 3.  
DR SMART: SM00409; Ig; 2.  
DR SMART: SM00407; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS50835; IG.LIKE; 4.  
DR PROSITE: PS00290; IG.MHC; UNKNOWN 2.  
DR Hypothetical protein.  
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCEDB81076E CRC64;

Query Match 90.8%; Score 1258; DB 2; Length 466;  
Best Local Similarity 100.0%; Pred. No. 4,1e-90;  
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHICPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
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Db 235 EPKSCDKHTKCPCPAPBELLGSPSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 294
Qy 61 NMTVDGEVHNATKTKREEDQNSTYRVSVLTVLHODMNGKSKYCKKCVSNKALPAPIEKT 120
Db 295 NMTVDGEVHNATKTKREEDQNSTYRVSVLTVLHODMNGKSKYCKKCVSNKALPAPIEKT 354
Qy 121 ISKAKGQPREPPQYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEMESNGQPENNYKTTTP 180
Db 355 ISKAKGQPREPPQYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEMESNGQPENNYKTTTP 414
Qy 181 PVLSDSGSFPLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPG 231
Db 415 PVLSDSGSFPLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPG 465

RESULT 6
Q727P5 PRELIMINARY; PRT; 469 AA.
ID 0727P5;
AC 0727P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RA Strausberg R.;
RA Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG-CL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-sec; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SO SEQUENCE 469 AA; 51395 MW; C0D5BE12BAAF795C CRC64;
Query Match 90.8%; Score 1258; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. No. 4; 2e-90;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 EPKSCDKHTKCPCPAPBELLGSPSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 238 EPKSCDKHTKCPCPAPBELLGSPSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 297
Qy 61 NMTVDGEVHNATKTKREEDQNSTYRVSVLTVLHODMNGKSKYCKKCVSNKALPAPIEKT 120
Db 298 NMTVDGEVHNATKTKREEDQNSTYRVSVLTVLHODMNGKSKYCKKCVSNKALPAPIEKT 357
Qy 121 ISKAKGQPREPPQYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEMESNGQPENNYKTTTP 180
Db 358 ISKAKGQPREPPQYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEMESNGQPENNYKTTTP 417
Qy 181 PVLSDSGSFPLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPG 231
Db 418 PVLSDSGSFPLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPG 468

RESULT 7
Q6RJA4 PRELIMINARY; PRT; 470 AA.
ID 06RJA4;
AC 06RJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG-CL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-sec; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
DR Hypothetical protein.
SO SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

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Query Match 90.8%; Score 1258; DB 2; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-90;  
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 DB 239 EPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298  
 QY 61 NMVYDGVVHNAKTKPREEQYNSTYRVSVLTVLHQMNLNGEKYCKVSNKALPAPIEKT 120  
 DB 299 NMVYDGVVHNAKTKPREEQYNSTYRVSVLTVLHQMNLNGEKYCKVSNKALPAPIEKT 358  
 QY 121 ISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 180  
 DB 359 ISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 418  
 QY 181 PVLSDSGSFLLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 231  
 DB 419 PVLSDSGSFLLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 469

RESULT 8  
 Q7ZSW1 PRELIMINARY; PRT; 470 AA.

ID Q7ZSW1  
 AC Q7ZSW1;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 GN NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schlier G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Diatchenko L., Marsina K., Moore T., Max S.T., Wang J., Hsieh L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzyzanski M.I., Skalka U., Smailus D.E., Schermer A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RU [2]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC053984; AAH53984.1; -.  
 DR HSSP: P01857; IHZH.  
 DR InterPro: IPR007110; IG\_1like.  
 DR InterPro: IPR003597; IG\_c1.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF07654; CI-set; 3.  
 DR SMART: SM00406; IGV; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.

KW Hypothetical protein.  
 SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;  
 Query Match 90.8%; Score 1258; DB 2; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-90;  
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 DB 239 EPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298  
 QY 61 NMVYDGVVHNAKTKPREEQYNSTYRVSVLTVLHQMNLNGEKYCKVSNKALPAPIEKT 120  
 DB 299 NMVYDGVVHNAKTKPREEQYNSTYRVSVLTVLHQMNLNGEKYCKVSNKALPAPIEKT 358  
 QY 121 ISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 180  
 DB 359 ISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 418  
 QY 181 PVLSDSGSFLLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 231  
 DB 419 PVLSDSGSFLLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 469

## RESULT 9

ID Q6N089 PRELIMINARY; PRT; 472 AA.

Q6N089  
 AC Q6N089;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Hypothetical protein DKFZp686P15220.  
 DE Hypothetical protein DKFZp686P15220.  
 GN Name=DKFZp686P15220;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 GN NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human rectum tumor;  
 RG The German Human cDNA Consortium;  
 RA Wambut R., Heubner D., Mewes H.W., Weill B., Amid C., Oeanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BX640627; CAB5781.1; -.  
 DR HSSP: P01861; IADQ.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG\_1like.  
 DR InterPro: IPR003597; IG\_c1.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF07654; CI-set; 3.  
 DR SMART: SM00409; IG; 2.  
 DR SMART: SM00407; IGcl; 3.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein  
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 90.8%; Score 1258; DB 2; Length 472;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-90;  
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 DB 241 EPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 300  
 QY 61 NMVYDGVVHNAKTKPREEQYNSTYRVSVLTVLHQMNLNGEKYCKVSNKALPAPIEKT 120  
 DB 301 NMVYDGVVHNAKTKPREEQYNSTYRVSVLTVLHQMNLNGEKYCKVSNKALPAPIEKT 360  
 QY 121 ISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 180

Db 361 ISKAKQPREPOYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNQPENNYKTTTP 420  
 Qy 181 PVLDSGSPFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKSLSPG 231  
 Db 421 PVLDSGSPFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKSLSPG 471

RESULT 10

OG6GM7 PRELIMINARY; PRT; 475 AA.  
 ID OG6GM7  
 AC OG6GM7  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Tothiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: BC073782; AAH73782.1; -.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003597; IG-cl.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF07654; Cl-sec; 3.  
 DR Pfam: PF00047; Ig; 4.  
 DR SMART: SM00409; Ig; 2.  
 DR SMART: SM00407; IgC1; 3.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PSS0835; IG LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

Query Match 90.8%; Score 1258; DB 2; Length 475;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-90;  
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTTCCPCAPABELLGGPSVFLPPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 60  
 Db 244 EPKSCDKHTTCCPCAPABELLGGPSVFLPPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKF 303

Qy 61 NTYVDGEVHNAKTKPREQYNSTYRVSVLTALHODMNLNGEKYCKCKVSKALPAPIEKT 120  
 Db 304 NTYVDGEVHNAKTKPREQYNSTYRVSVLTALHODMNLNGEKYCKCKVSKALPAPIEKT 363  
 Qy 121 ISKAKQPREPOYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNQPENNYKTTTP 180  
 Db 364 ISKAKQPREPOYYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNQPENNYKTTTP 423

RESULT 11

OG6GM7 PRELIMINARY; PRT; 476 AA.  
 ID OG6GM7  
 AC OG6GM7  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Tothiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: BC073773; AAH73773.1; -.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003597; IG-cl.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF07654; Cl-sec; 3.  
 DR Pfam: PF00047; Ig; 4.  
 DR SMART: SM00409; Ig; 2.  
 DR SMART: SM00407; IgC1; 3.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PSS0835; IG LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 476 AA; 52286 MW; 622AAB5C62DDE9D CRC64;

Query Match 90.8%; Score 1258; DB 2; Length 476;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-90;  
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCAPAPBLGSPVFLPPPKKDTLMIISRTPEVTCVVDVSHEDPEVKF 60  
 DB 245 EPKSCDKHTHTCPPCAPAPBLGSPVFLPPPKKDTLMIISRTPEVTCVVDVSHEDPEVKF 304  
 QY 61 NMVYDGEVHNNAKTPREBQVNSTRYVSVLTVLHODMLNKEKYCKVSNKALPAPLEKT 120  
 DB 305 NMVYDGEVHNNAKTPREBQVNSTRYVSVLTVLHODMLNKEKYCKVSNKALPAPLEKT 364  
 QY 121 ISKAKGQPREPQVYTLPPSRDELITKNQVSLTCLVKGFPSPDIAVWESNGQPENNYKTFP 180  
 DB 365 ISKAKGQPREPQVYTLPPSRDELITKNQVSLTCLVKGFPSPDIAVWESNGQPENNYKTFP 424  
 QY 181 PVLDSDGSFPLYSKLTVDKSRMOQGNVFCSVNHEALHNHYTKSLSPG 231  
 DB 425 PVLDSDGSFPLYSKLTVDKSRMOQGNVFCSVNHEALHNHYTKSLSPG 475

## RESULT 12

Q96P08 PRELIMINARY; PRT; 679 AA.

AC Q96P08; 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Factor VII active site mutant immunocoujugate.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NC NCB1\_Taxid=9606;  
 RX SEQUENCE FROM N.A. MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;  
 RT "Targeting tissue factor on tumor vascular endothelial cells and tumor  
 Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Hu Z., Garen A.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF272774; AAK58686.2; -  
 DR HSSP; P08709; IGLI.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004235; F:trypsin activity; IEA.  
 DR GO; GO:000508; F:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000152; Aex\_Hydroxyl\_5.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_Like.  
 DR InterPro; IPR007110; IG-1-like.  
 DR InterPro; IPR003597; IG-1-like.  
 DR InterPro; IPR003006; IG-MHC.  
 DR InterPro; IPR001254; Peptidase S1.  
 DR InterPro; IPR009003; Pept\_ser\_Cys.  
 DR InterPro; IPR000294; VitK\_dep\_Gla.  
 DR Pfam; PF07654; Cl-sec; 2.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF00594; Gla; 1.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00069; Gla; 1.  
 DR SMART; SM00407; IGLI; 1.  
 DR SMART; SM00020; TYP\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS0186; EGF\_2; 1.  
 DR PROSITE; PS00026; EGF\_3; 1.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; Gla\_1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 DR PROSITE; PS0240; TRYPsin\_DOM; 1.  
 DR PROSITE; PS00134; TRYPsin\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPsin\_SER; 1.  
 DR EGF-like domain; Hydroxylase; Protease; Serine protease.  
 KW EGF-like domain; Hydroxylase; Protease; Serine protease.  
 SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;

Query Match 90.84; Score 1258; DB 2; Length 679;  
 Best local similarity 100.0%; Freq. No. 6; 6e-90;  
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPPCAPAPBLGSPVFLPPPKKDTLMIISRTPEVTCVVDVSHEDPEVKF 60  
 DB 448 EPKSCDKHTHTCPPCAPAPBLGSPVFLPPPKKDTLMIISRTPEVTCVVDVSHEDPEVKF 507  
 QY 61 NMVYDGEVHNNAKTPREBQVNSTRYVSVLTVLHODMLNKEKYCKVSNKALPAPLEKT 120  
 DB 508 NMVYDGEVHNNAKTPREBQVNSTRYVSVLTVLHODMLNKEKYCKVSNKALPAPLEKT 567  
 QY 121 ISKAKGQPREPQVYTLPPSRDELITKNQVSLTCLVKGFPSPDIAVWESNGQPENNYKTFP 180  
 DB 568 ISKAKGQPREPQVYTLPPSRDELITKNQVSLTCLVKGFPSPDIAVWESNGQPENNYKTFP 627  
 QY 181 PVLDSDGSFPLYSKLTVDKSRMOQGNVFCSVNHEALHNHYTKSLSPG 231  
 DB 628 PVLDSDGSFPLYSKLTVDKSRMOQGNVFCSVNHEALHNHYTKSLSPG 678

## RESULT 13

Q6P055 PRELIMINARY; PRT; 473 AA.

AC Q6P055; 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NC NCB1\_Taxid=9606;  
 RX SEQUENCE FROM N.A. TISSUE-Peripheral Nervous System; DOI=10.1073/pnas.242638999;  
 RC MEDLINE=22388257; PubMed=12477932; -  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Berger J.G.,  
 RA Strausberg R.L., Colling B.S., Wagner L., Shenmen C.F., Bhat N.K.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Matrusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Cantucci P., Mullaly S.J.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Maler J.A., Hulyk S.W.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Gay L.J., Hulyk S.W.,  
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villard D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skaleka U., Smalins D.E., Schermer A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A. TISSUE-Peripheral Nervous System;  
 RC Strausberg R.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC065820; AAH65820.1; -  
 DR HSSP; P01861; IADO.  
 DR InterPro; IPR003599; IG-1-like.  
 DR InterPro; IPR007110; IG-1-like.



DR InterPro: IPR003597; Ig\_C1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF07654; CI-set; 3.  
 DR SMART: SM00409; Ig; 2.  
 DR SMART: SM00407; IgC1; 3.  
 DR PROSITE: PS00835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 DR Hypothetical protein.  
 KW SEQUENCE 475 AA; 51344 MW; 9816D56477129857 CRC64;

Query Match 90.5%; Score 1254; DB 2; Length 473;  
 Best Local Similarity 99.6%; Pred. No. 8.7e-90;  
 Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPKSCDKHTTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 60  
 DB 242 EPKSCDKHTTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 301  
 QY 61 NMVVGVEVHNAKTKRREQYSTYRVSVLTVLHODMNGKRYCKKVSNNKALPAPIEKT 120  
 DB 302 NMVVGVEVHNAKTKRREQYSTYRVSVLTVLHODMNGKRYCKKVSNNKALPAPIEKT 361  
 QY 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQEPENNYKTT 180  
 DB 362 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQEPENNYKTT 421  
 QY 181 PVLDSGSEFFLYSKLTVDKSRWQGNVFSCSVHREALHNHYTQKSLSLSPG 231  
 DB 422 PVLDSGSEFFLYSKLTVDKSRWQGNVFSCSVHREALHNHYTQKSLSLSPG 472

## RESULT 14

Q6MZ06 PRELIMINARY; PRT; 475 AA.  
 AC 06MZ06;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein DKFZp686G11190.  
 GN Name=DKFZp686G11190;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human esophagus tumor;  
 RG The German Human CDNA Consortium;  
 RA Lauber U., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,  
 RA Han M., Wiemann S.;  
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BX640947; CAB45972.1; -.  
 DR HSSP: P01861; IADO.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig\_C1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF07654; CI-set; 3.  
 DR SMART: SM00409; Ig; 2.  
 DR SMART: SM00407; IgC1; 3.  
 DR SMART: SM00406; IgV; 1.  
 DR PROSITE: PS00835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 DR Hypothetical protein.  
 KW SEQUENCE 475 AA; 52043 MW; B7EAB255A26F48E CRC64;

Query Match 90.5%; Score 1254; DB 2; Length 475;  
 Best Local Similarity 99.6%; Pred. No. 8.7e-90;  
 Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPKSCDKHTTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 60  
 DB 244 EPKSCDKHTTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 303  
 QY 61 NMVVGVEVHNAKTKRREQYSTYRVSVLTVLHODMNGKRYCKKVSNNKALPAPIEKT 120  
 DB 304 NMVVGVEVHNAKTKRREQYSTYRVSVLTVLHODMNGKRYCKKVSNNKALPAPIEKT 363  
 QY 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQEPENNYKTT 180  
 DB 364 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQEPENNYKTT 423  
 QY 181 PVLDSGSEFFLYSKLTVDKSRWQGNVFSCSVHREALHNHYTQKSLSLSPG 231  
 DB 424 PVLDSGSEFFLYSKLTVDKSRWQGNVFSCSVHREALHNHYTQKSLSLSPG 474

## RESULT 15

Q6N094 PRELIMINARY; PRT; 480 AA.  
 AC 06N094;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein DKFZp686O01196.  
 GN Name=DKFZp686O01196;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human esophagus tumor;  
 RG The German Human CDNA Consortium;  
 RA Wambut R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BX640622; CAB45776.1; -.  
 DR HSSP: P01861; IADO.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig\_C1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF07654; CI-set; 3.  
 DR SMART: SM00409; Ig; 2.  
 DR SMART: SM00407; IgC1; 3.  
 DR SMART: SM00406; IgV; 1.  
 DR PROSITE: PS00835; IG\_LIKE; 4.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein  
 KW SEQUENCE 480 AA; 2252473D35AEC18 CRC64;

Query Match 90.5%; Score 1254; DB 2; Length 480;  
 Best Local Similarity 99.6%; Pred. No. 8.8e-90;  
 Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPKSCDKHTTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 60  
 DB 249 EPKSCDKHTTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 308  
 QY 61 NMVVGVEVHNAKTKRREQYSTYRVSVLTVLHODMNGKRYCKKVSNNKALPAPIEKT 120  
 DB 309 NMVVGVEVHNAKTKRREQYSTYRVSVLTVLHODMNGKRYCKKVSNNKALPAPIEKT 368  
 QY 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQEPENNYKTT 180  
 DB 369 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQEPENNYKTT 428  
 QY 181 PVLDSGSEFFLYSKLTVDKSRWQGNVFSCSVHREALHNHYTQKSLSLSPG 231  
 DB 429 PVLDSGSEFFLYSKLTVDKSRWQGNVFSCSVHREALHNHYTQKSLSLSPG 479

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